

GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:20:06 ; Search time 0.001 Seconds

(without alignments)
858.346 Million cell updates/sec

Title: us-09-488-265-26

Perfect score: 2470

Sequence: 1 MGVEVLLSLATLFGSTGALPGRGNHSCDVTGQYGCPEISHLMGQYSPFFSLADE 467

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: ramirez126.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2470	100.0	467	1	US-09-343-126C-129
2	2448	99.1	467	1	US-09-343-126C-134
3	2342	94.8	467	1	US-09-343-126C-132
4	2115	85.6	437	1	US-09-343-126C-130

ALIGNMENTS

RESULT 1

US-09-343-126C-129

; Sequence 129, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-129

Query Match 100.0%; Score 2470; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGVEVLLSLATLFGSTGALPGRGNHSCDVTGQYGCPEISHLMGQYSPFFSLADE 60

Db 1 MGVEVLLSLATLFGSTGALPGRGNHSCDVTGQYGCPEISHLMGQYSPFFSLADE 60
OY 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKYSALIAIOMNATAFKGYAFLEKTYN 120
Db 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKYSALIAIOMNATAFKGYAFLEKTYN 120
OY 121 YTLGADDLTPFGEOOMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
Db 121 YTLGADDLTPFGEOOMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
OY 181 KLADPGANPHQASPVINVIIEGAGYNNLTLDHGLCTAFEESELDGDDVEANFTAVFAPR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNLTLDHGLCTAFEESELDGDDVEANFTAVFAPR 240
OY 241 ARLEAHLPGVNLTDEDDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300
Db 241 ARLEAHLPGVNLTDEDDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300
OY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNTTLDNPAATPLNATLYADS 360
Db 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVODHTSTNTTLDNPAATPLNATLYADS 360
OY 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPBARAYEMQCEAEKEP 420
Db 361 HDNTMWSIFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPBARAYEMQCEAEKEP 420
OY 421 LVRLVNDRVVPLHGGGVKDLGRCKRDPFEGLSFARSNGNMECEFA 467
Db 421 LVRLVNDRVVPLHGGGVKDLGRCKRDPFEGLSFARSNGNMECEFA 467

RESULT 2

US-09-343-126C-134

; Sequence 134, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-134

Query Match 99.1%; Score 2448; DB 1; Length 467;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 462; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MGVEVLLSLATLFGSTGALPGRGNHSCDVTGQYGCPEISHLMGQYSPFFSLADE 60
Db 1 MGVEVLLSLATLFGSTGALPGRGNHSCDVTGQYGCPEISHLMGQYSPFFSLADE 60
OY 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKYSALIAIOMNATAFKGYAFLEKTYN 120
Db 61 SAISPDVPRKGRVTFVQVLSRHGARYPTSSKSKYSALIAIOMNATAFKGYAFLEKTYN 120
OY 121 YTLGADDLTPFGEOOMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
Db 121 YTLGADDLTPFGEOOMVNSGKIFRRYKALARKIVPEVRASGSDRVYASAEKEIEGQSA 180
OY 181 KLADPGANPHQASPVINVIIEGAGYNNLTLDHGLCTAFEESELDGDDVEANFTAVFAPR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNLTLDHGLCTAFEESELDGDDVEANFTAVFAPR 240
OY 241 ARLEAHLPGVNLTDEDDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300
Db 241 ARLEAHLPGVNLTDEDDVNNLMDKCPFTVARTSDATQLSFCDLFTHDEWIOYDYLSIG 300

Db 241 ARLEAHLPGVNLDEEDVYNLMDCPEFDVARTSDATQLSPECDLFTHDEMIQDYDLSIG 300
QY 301 KYIYGAGNPLGPAQGVGVNELLARLTHSPQDHTSTNHTLDSNPATPLNATLYADFS 360
Db 301 KYIYGAGNPLGPAQGVGVNELLARLTHSPQDHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HNDTWISIFPALGLYNGTPLSTTSVESIEETDGYAASWTPFARAYVEMMOCEAKEP 420
Db 361 HNDTWISIFPALGLYNGTPLSTTSVESIEETDGYAASWTPFARAYVEMMOCEAKEP 420
QY 421 LVRVLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGGNMBCEFA 467
Db 421 LVRVLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGGNMBCEFA 467
RESULT 3
US-09-343-126C-132
; Sequence 132, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-132

Query Match 94.8%; Score 2342; DB 1; Length 467;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 441; Conservative 10; Mismatches 16; Indels 0; Gaps 0;
QY 1 MGCVVVLISATLFGSTSGTALGPRGNSHSDTVDGQYQCFPEISHLMGQYSPFSLADE 60
Db 1 MGCVVVLISATLFGSTSGTALGPRGNSHSDTVDGQYQCFPEISHLMGQYSPFSLADE 60
QY 61 SAISPDVPGKGRVTFVOYLSRHGARYPTSSSKSKYTSALIRAIQKNATAFKGYAFLKTYN 120
Db 61 SAISPDVPGKGRVTFVOYLSRHGARYPTSSSKSKYTSALIRAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEOQWVNSGKIFKFRKALARKIVPFIRASGSDRVIASAEKIEGQSA 180
Db 121 YTLGADDLTPFGEOQWVNSGKIFKFRKALARKIVPFIRASGSDRVIASAEKIEGQSA 180
QY 121 YTLGADDLTPFGEOQWVNSGKIFKFRKALARKIVPFIRASGSDRVIASAEKIEGQSA 180
Db 121 YTLGADDLTPFGEOQWVNSGKIFKFRKALARKIVPFIRASGSDRVIASAEKIEGQSA 180
QY 181 KLADPGANPHQASPIYINVIIEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGANPHQASPIYINVIIEGAGYNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLDEEDVYNLMDCPEFDVARTSDATQLSPECDLFTHDEMIQDYDLSIG 300
Db 241 ARLEAHLPGVNLDEEDVYNLMDCPEFDVARTSDATQLSPECDLFTHDEMIQDYDLSIG 300
QY 301 KYIYGAGNPLGPAQGVGVNELLARLTHSPQDHTSTNHTLDSNPATPLNATLYADFS 360
Db 301 KYIYGAGNPLGPAQGVGVNELLARLTHSPQDHTSTNHTLDSNPATPLNATLYADFS 360
QY 361 HNDTWISIFPALGLYNGTPLSTTSVESIEETDGYAASWTPFARAYVEMMOCEAKEP 420
Db 361 HNDTWISIFPALGLYNGTPLSTTSVESIEETDGYAASWTPFARAYVEMMOCEAKEP 420
QY 421 LVRVLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGGNMBCEFA 467
Db 421 LVRVLVNDRVVPLHGGCVGVDKLGCRKRDVEGLSFARSGGNMBCEFA 467

RESULT 4
US-09-343-126C-130

; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

Query Match 85.6%; Score 2115; DB 1; Length 437;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 419; Conservative 2; Mismatches 9; Indels 18; Gaps 10;
QY 27 NSHSCDVIYDGQYQCFPEISHLMGQYSPFSLADESAISPDVPGKGRVTFVOYLSRHGARY 86
Db 1 NSHSCDVIYDGQYQCFPEISHLMGQYSPFSLADESAISPDVPGKGRVTFVOYLSRHGARY 86
QY 87 PTSSSKSKYTSALIRAIQKNATAFKGYAFLKTYNVTGADDLTPFGEOQWVNSGKIFKTYR 146
Db 59 PTSSSKSKYTSALIRAIQKNATAFKGYAFLKTYNVTGADDLTPFGEOQWVNSGKIFKTYR 117
QY 147 YKALARKIVPFIRASGSDRVIASAEKIEGQSAKLADPGANPHQASPIYINVIIEGAGY 206
Db 118 YKALARKIVPFIRASGSDRVIASAEKIEGQSAKLADPGANPHQASPIYINVIIEGAGY 174
QY 207 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARIARLEAHLPGVNLDEEDVYNLMDCPE 266
Db 175 NNTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARIARLEAHLPGVNLDEEDVYNLMDCPE 233
QY 267 DTVARTSDATQLSPECDLFTHDEMIQDYDLSIGKRYGAGNPLGPAQGVGVNELLAR 326
Db 234 DTVARTSDATQLSPECDLFTHDEMIQDYDLSIGKRYGAGNPLGPAQGVGVNELLAR 290
QY 327 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSHNDTWISIFPALGLYNGTPLSTTSV 386
Db 291 LTHSPVQDHTSTNHTLDSNPATPLNATLYADFSHNDTWISIFPALGLYNGTPLSTTSV 350
QY 387 ESIEETDGYAASWTPFARAYVEMMOCEA-----EKEPLVRLVNDRVVPLHGGCVD 439
Db 351 ESIEETDGYAASWTPFARAYVEMMOCEA-----EKEPLVRLVNDRVVPLHGGCVD 409
QY 440 KLGRCKRDDVEGLSFARSGGNMBCEFA 467
Db 410 KLGRCKRDDVEGLSFARSGGNMBCEFA 437

Search completed: March 20, 2003, 08:20:07
Job time: 1 sec

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:22:01 ; Search time 0.001 Seconds

(without alignments)
803.206 Million cell updates/sec

Title: us-09-488-265-27

Perfect score: 2321

Sequence: 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVEVQVLSRHGARYPT 437

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 4 seqs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ramirez126.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2321	100.0%	437	1	US-09-343-126C-130
2	2115	91.1%	467	1	US-09-343-126C-129
3	2093	90.2%	467	1	US-09-343-126C-134
4	2044	88.1%	467	1	US-09-343-126C-132

ALIGNMENTS

RESULT 1
US-09-343-126C-130
; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

Query Match 100.0%; Score 2321; DB 1; Length 437;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 437; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVEVQVLSRHGARYPT 60

Db 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVEVQVLSRHGARYPT 60
QY 61 SSKSKKYSALLERIOKNATFKKRYAFLKTYNTTLCADDLTPGEGNOMVNSGKIFYRRYA 120
Db 61 SSKSKKYSALLERIOKNATFKKRYAFLKTYNTTLCADDLTPGEGNOMVNSGKIFYRRYA 120
QY 121 IARNIVPEVRASGSDRVIASAEKFEFGOSAKLADPAHQASPVTVIIPESGGYNNLTDDH 180
Db 121 IARNIVPEVRASGSDRVIASAEKFEFGOSAKLADPAHQASPVTVIIPESGGYNNLTDDH 180
QY 181 GLCTAFEDSTIGDDEANFTAFAPPIRARLEALPGVNLTDDEVYNNLMDMCPDVTARTS 240
Db 181 GLCTAFEDSTIGDDEANFTAFAPPIRARLEALPGVNLTDDEVYNNLMDMCPDVTARTS 240
QY 241 DATOLSPFCDLFTADEWQYDYLOSILKYYGAGNPGLGACVGNELIARLTSPVDHT 300
Db 241 DATOLSPFCDLFTADEWQYDYLOSILKYYGAGNPGLGACVGNELIARLTSPVDHT 300
QY 301 STNHTLDSNPATFPPLNATLYADFSHDNTMVSIFPALGLYNGTKPLSTTSVESIETDGYAA 360
Db 301 STNHTLDSNPATFPPLNATLYADFSHDNTMVSIFPALGLYNGTKPLSTTSVESIETDGYAA 360
QY 361 SWTVPFARAYVEMMOCCAGGGGGBEKEPLRVRLVNDRVVPLHGGGVKLGKCKLDDFV 420
Db 361 SWTVPFARAYVEMMOCCAGGGGGBEKEPLRVRLVNDRVVPLHGGGVKLGKCKLDDFV 420
QY 421 EGLSFARSGGNMAECFA 437
Db 421 EGLSFARSGGNMAECFA 437

RESULT 2
US-09-343-126C-129
; Sequence 129, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-129

Query Match 91.1%; Score 2115; DB 1; Length 467;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 419; Conservative 2; Mismatches 9; Indels 16; Gaps 10;

QY 1 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVEVQVLSRHGARY 58
Db 27 NSHSCDVTVDGYQCPEISHLMGOYSPFFSLADESAISPDPVKGCRTVEVQVLSRHGARY 86
QY 59 PTSSKSKYSALLERIOKNATFKKRYAFLKTYNTTLCADDLTPGEGNOMVNSGKIFYRR 117
Db 59 PTSSKSKYSALLERIOKNATFKKRYAFLKTYNTTLCADDLTPGEGNOMVNSGKIFYRR 117
QY 87 PTSSKSKYSALLERIOKNATFKKRYAFLKTYNTTLCADDLTPGEGNOMVNSGKIFYRR 146
Db 87 PTSSKSKYSALLERIOKNATFKKRYAFLKTYNTTLCADDLTPGEGNOMVNSGKIFYRR 146
QY 118 YKALARNIVPEVRASGSDRVIASAEKFEFGOSAKLADPAHQASPVTVIIPESGGY 174
Db 147 YKALARNIVPEVRASGSDRVIASAEKFEFGOSAKLADPAHQASPVTVIIPESGGY 206
QY 175 NNTLHDGICTAPEFDSLTGDAEANTFVAPPRARLEA-LRQVNLTDDEVYNNLMDMCP 233
Db 207 NNTLHDGICTAPEFDSLTGDAEANTFVAPPRARLEA-LRQVNLTDDEVYNNLMDMCP 266
QY 234 DTAFTSDATOLSPFCDLFTADEW-QDYLOSILKYYGAGNPGLGACVGNELIAR 290

Db 267 DTVAATSDATQUSPCDCLFTHDEMTQYDYLQSLGKYYGAGNPLGPAQGVGFVNNELIAR 326
QY 291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSV 350
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSV 386
QY 351 EST-ETDGYAASWTPFAARAIVEMMOCEAGGGEKEPELVRLVNDRVVPLHGGVD 409
Db 387 ESTETDGYAASWTPFAARAIVEMMOCEA-----EKEPLVRLVNDRVVPLHGGVD 439
QY 410 KLGRCKLDPEVEGLSFARSGNMMAECFA 437
Db 440 KLGRCKRDPFVEGLSFARSGNMMECEFA 467

RESULT 3
US-09-343-126C-134
; Sequence 134, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 134
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-134

Query Match 90.2%; Score 2093; DB 1; Length 467;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 414; Conservative 4; Mismatches 12; Indels 18; Gaps 10;

QY 1 NSHSCDHYD-GYOC-PEISHLMGQYSPFSLADESAISPDVPGCRVTFVQVLSRHGARY 58
Db 27 NSHSCDHYDGYOCPEISHLMGQYSPFSLADESAISPDVPGCRVTFVQVLSRHGARY 86
QY 59 PTSSKSKYSALIERIOKNAT-FKGYAFLKTYNTYLGAADLPPFGENQMVNSGKIFRYR 117
Db 87 PTSSASAKYSALIERIOKNATFAKGYAFLKTYNTYLGAADLPPFGENQMVNSGKIFRYR 146
QY 118 YKALARNIVPFVRASGSDRYIASAEKFEIGFOSAKLADPA---HQASPVINVIIPESGY 174
Db 147 YKALARKIVPFIRASGSDRYIASAEKFEIGFOSAKLADPGANPHQASPVINVIIPESGAGY 206
QY 175 NNTLDHGLCTAFEDSTIGDGAENFTAVFAPPIRARLEA-LPGVNLDEDEVNLMDCPF 233
Db 207 NNTLDHGLCTAFEDSELGDVEANFTAVFAPPIRARLEALPGVNLDEDEVNLMDCPF 266
QY 234 DTVAATSDATQUSPCDCLFTHADEM-QYDYLOSL-KYYGYAGNPLGPAQGVGF-NELIAR 290
Db 267 DTVAATSDATQUSPCDCLFTHADEMIOYDYLQSLGKYYGAGNPLGPAQGVGFVNNELIAR 326
QY 291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSV 350
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSV 386
QY 351 EST-ETDGYAASWTPFAARAIVEMMOCEAGGGEKEPELVRLVNDRVVPLHGGVD 409
Db 387 ESTETDGYAASWTPFAARAIVEMMOCEA-----EKEPLVRLVNDRVVPLHGGVD 439
QY 410 KLGRCKLDPEVEGLSFARSGNMMAECFA 437
Db 440 KLGRCKRDPFVEGLSFARSGNMMECEFA 467

RESULT 4
US-09-343-126C-132

; Sequence 132, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-132

Query Match 88.1%; Score 2044; DB 1; Length 467;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 405; Conservative 7; Mismatches 18; Indels 18; Gaps 10;

QY 1 NSHSCDHYD-GYOC-PEISHLMGQYSPFSLADESAISPDVPGCRVTFVQVLSRHGARY 58
Db 27 NSHSCDHYDGYOCPEISHLMGQYSPFSLADESAISPDVPGCRVTFVQVLSRHGARY 86
QY 59 PTSSKSKYSALIERIOKNAT-FKGYAFLKTYNTYLGAADLPPFGENQMVNSGKIFRYR 117
Db 87 PTSSASAKYSALIERIOKNATFAKGYAFLKTYNTYLGAADLPPFGENQMVNSGKIFRYR 146
QY 118 YKALARNIVPFVRASGSDRYIASAEKFEIGFOSAKLADPA---HQASPVINVIIPESGY 174
Db 147 YKALARKIVPFIRASGSDRYIASAEKFEIGFOSAKLADPGANPHQASPVINVIIPESGAGY 206
QY 175 NNTLDHGLCTAFEDSTIGDGAENFTAVFAPPIRARLEA-LPGVNLDEDEVNLMDCPF 233
Db 207 NNTLDHGLCTAFEDSELGDVEANFTAVFAPPIRARLEALPGVNLDEDEVNLMDCPF 266
QY 234 DTVAATSDATQUSPCDCLFTHADEM-QYDYLOSL-KYYGYAGNPLGPAQGVGF-NELIAR 290
Db 267 DTVAATSDATQUSPCDCLFTHADEMIOYDYLQSLGKYYGAGNPLGPAQGVGFVNNELIAR 326
QY 291 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSV 350
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSV 386
QY 351 EST-ETDGYAASWTPFAARAIVEMMOCEAGGGEKEPELVRLVNDRVVPLHGGVD 409
Db 387 ESTETDGYAASWTPFAARAIVEMMOCEA-----EKEPLVRLVNDRVVPLHGGVD 439
QY 410 KLGRCKLDPEVEGLSFARSGNMMAECFA 437
Db 440 KLGRCKRDPFVEGLSFARSGNMMECEFA 467

Search completed: March 20, 2003, 08:22:01
Job time : 0.001 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 20, 2003, 08:23:05 ; Search time 0.001 Seconds

(without alignments)

858.346 Million cell updates/sec

Title: us-09-488-265-29

Perfect score: 2462

Sequence: 1 MGFFVLLSTATLFGSTSGTALGP...DEVEGLSFARSGGMAECFA 467

Scoring table: BLOSUM62

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Searched: 4 seqs, 1838 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: ramirez126.pep.*

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2462	100.0	467	1	US-09-343-126C-132
2	2362	95.9	467	1	US-09-343-126C-134
3	2342	95.1	467	1	US-09-343-126C-129
4	2044	83.0	437	1	US-09-343-126C-130

ALIGNMENTS

RESULT 1
US-09-343-126C-132

; Sequence 132, Application US/09343126C

; GENERAL INFORMATION:

; APPLICANT: Brugger, Roland

; APPLICANT: Lehmann, Martin

; APPLICANT: Wysz, Markus

; TITLE OF INVENTION: Phytase Formulations

; FILE REFERENCE: C38435/109741

; CURRENT APPLICATION NUMBER: US/09/343.126C

; CURRENT FILING DATE: 1999-06-29

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 132

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Consensus sequence

US-09-343-126C-132

Query Match 100.0%; Score 2462; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFFVLLSTATLFGSTSGTALGP...DEVEGLSFARSGGMAECFA 60

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Db      1 MGFFVLLSTATLFGSTSGTALGP...DEVEGLSFARSGGMAECFA 60
QY      1 MGFFVLLSTATLFGSTSGTALGP...DEVEGLSFARSGGMAECFA 60
Db      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEIAIOKNATAFKGYAFLTKYN 120
QY      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEIAIOKNATAFKGYAFLTKYN 120
Db      121 YTLGADDLTFPGENQVNSGIFKFRYKALAKIYVFIASGSDRYASAEKFIQFQSA 180
QY      121 YTLGADDLTFPGENQVNSGIFKFRYKALAKIYVFIASGSDRYASAEKFIQFQSA 180
Db      122 YTLGADDLTFPGENQVNSGIFKFRYKALAKIYVFIASGSDRYASAEKFIQFQSA 180
QY      122 YTLGADDLTFPGENQVNSGIFKFRYKALAKIYVFIASGSDRYASAEKFIQFQSA 180
Db      181 KLADPGSOPHOASPVYINVIIPESGYNNTLDHGTCTAFEDSELGDVDFANFALFAPAIR 240
QY      181 KLADPGSOPHOASPVYINVIIPESGYNNTLDHGTCTAFEDSELGDVDFANFALFAPAIR 240
Db      182 KLADPGSOPHOASPVYINVIIPESGYNNTLDHGTCTAFEDSELGDVDFANFALFAPAIR 240
QY      182 KLADPGSOPHOASPVYINVIIPESGYNNTLDHGTCTAFEDSELGDVDFANFALFAPAIR 240
Db      241 ARLEADLPQVTLTDEEDVYILMDMCPEDVARTSDATELSPFCALFTHDEWIQDYLSIG 300
QY      241 ARLEADLPQVTLTDEEDVYILMDMCPEDVARTSDATELSPFCALFTHDEWIQDYLSIG 300
Db      301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTNNHLLDSNPATFPLNATLYADF 360
QY      301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTNNHLLDSNPATFPLNATLYADF 360
Db      361 HDNTMISIFPALGLYNGTKPLSTTSVESIEETDGYASWTPFARAVEMQOAEKEP 420
QY      361 HDNTMISIFPALGLYNGTKPLSTTSVESIEETDGYASWTPFARAVEMQOAEKEP 420
Db      421 LVRVLVNDRVVPLHGCAYDKLGRCKRDFEVLGSLFARSGGMAECFA 467
QY      421 LVRVLVNDRVVPLHGCAYDKLGRCKRDFEVLGSLFARSGGMAECFA 467
Db      467 LVRVLVNDRVVPLHGCAYDKLGRCKRDFEVLGSLFARSGGMAECFA 467

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RESULT 2

US-09-343-126C-134

; Sequence 134, Application US/09343126C

; GENERAL INFORMATION:

; APPLICANT: Brugger, Roland

; APPLICANT: Lehmann, Martin

; APPLICANT: Wysz, Markus

; TITLE OF INVENTION: Phytase Formulations

; FILE REFERENCE: C38435/109741

; CURRENT APPLICATION NUMBER: US/09/343.126C

; CURRENT FILING DATE: 1999-06-29

; NUMBER OF SEQ ID NOS: 139

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 134

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Consensus sequence

US-09-343-126C-134

Query Match 95.9%; Score 2362; DB 1; Length 467;
Best Local Similarity 95.5%; Pred. No. 0;

Matches 446; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

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QY      1 MGFFVLLSTATLFGSTSGTALGP...DEVEGLSFARSGGMAECFA 60
Db      1 MGFFVLLSTATLFGSTSGTALGP...DEVEGLSFARSGGMAECFA 60
QY      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEIAIOKNATAFKGYAFLTKYN 120
Db      61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKVSALEIAIOKNATAFKGYAFLTKYN 120
QY      121 YTLGADDLTFPGENQVNSGIFKFRYKALAKIYVFIASGSDRYASAEKFIQFQSA 180
Db      121 YTLGADDLTFPGENQVNSGIFKFRYKALAKIYVFIASGSDRYASAEKFIQFQSA 180
QY      181 KLADPGSOPHOASPVYINVIIPESGYNNTLDHGTCTAFEDSELGDVDFANFALFAPAIR 240
Db      181 KLADPGSOPHOASPVYINVIIPESGYNNTLDHGTCTAFEDSELGDVDFANFALFAPAIR 240
QY      241 ARLEADLPQVTLTDEEDVYILMDMCPEDVARTSDATELSPFCALFTHDEWIQDYLSIG 300
Db      241 ARLEADLPQVTLTDEEDVYILMDMCPEDVARTSDATELSPFCALFTHDEWIQDYLSIG 300

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; Sequence 129, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Bruggen, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
; US-09-343-126C-129

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Query Match
Best Local Similarity 94.4%; Pred. No. 0;
Matches 441; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Bruggen, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
; US-09-343-126C-130

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RESULT 4
US-09-343-126C-130

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; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Bruggen, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wyss, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343,126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
; US-09-343-126C-130

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Search completed: March 20, 2003, 08:23:06
Job time : 0.001 secs


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Db 241 ARLEAHLPGVNLDEDEVYVNLMDMCPDTVARTSDATQLSFCDLFTHDEWIQYDIQSLG 300
; Sequence 132, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wysz, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343.126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 132
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-132

Query Match          95.7%; Score 2362; DB 1; Length 467;
Best Local Similarity 95.5%; Pred. No. 0;
Matches 446; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MGVEFVLLSTALFGSTSGTALGPRGNHSCDTPVDSGYOCFPEISHLMGTSPFSLADE 60
Db 1 MGVEFVLLSTALFGSTSGTALGPRGNHSCDTPVDSGYOCFPEISHLMGTSPFSLADE 60
QY 61 SAISPDVPGKRTFVVOVLSRHGARYPTSSASKAYSALEIOLKNTAFKGYAFLKTYN 120
Db 61 SAISPDVPGKRTFVVOVLSRHGARYPTSSASKAYSALEIOLKNTAFKGYAFLKTYN 120
QY 121 YTGADDLTPFGEQOQVNSGIRKRYRYKALAKIYPPIRASGSDRYIASSEKIEBQSA 180
Db 121 YTGADDLTPFGEQOQVNSGIRKRYRYKALAKIYPPIRASGSDRYIASSEKIEBQSA 180
QY 181 KLAPOGANPHQASPVIVITPEAGYNTLTDHGLCTAFEESELDGDDVEANFTAVFAPPIR 240
Db 181 KLAPOGANPHQASPVIVITPEAGYNTLTDHGLCTAFEESELDGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNLDEDEVYVNLMDMCPDTVARTSDATQLSFCDLFTHDEWIQYDIQSLG 300
Db 241 ARLEAHLPGVNLDEDEVYVNLMDMCPDTVARTSDATQLSFCDLFTHDEWIQYDIQSLG 300
QY 301 KYTGAGNPLGPAQGVGFVVELLARTLHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYTGAGNPLGPAQGVGFVVELLARTLHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
QY 361 HDNMTVSIFFFALGLXNGKPLSTSVESIEETDGYASWTVFAARAYVEMMOCEAKEP 420
Db 361 HDNMTVSIFFFALGLXNGKPLSTSVESIEETDGYASWTVFAARAYVEMMOCEAKEP 420
QY 421 LVRVLVNDRVVPLHGGVDKLGRCRDDFVHGLSFARSGGWMECEFA 467
Db 421 LVRVLVNDRVVPLHGGVDKLGRCRDDFVHGLSFARSGGWMECEFA 467

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RESULT 4
US-09-343-126C-130

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; Sequence 130, Application US/09343126C
; GENERAL INFORMATION:
; APPLICANT: Brugger, Roland
; APPLICANT: Lehmann, Martin
; APPLICANT: Wysz, Markus
; TITLE OF INVENTION: Phytase Formulations
; FILE REFERENCE: C38435/109741
; CURRENT APPLICATION NUMBER: US/09/343.126C
; CURRENT FILING DATE: 1999-06-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 130
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Consensus sequence
US-09-343-126C-130

Query Match          84.8%; Score 2093; DB 1; Length 437;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 414; Conservative 4; Mismatches 12; Indels 18; Gaps 10;

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QY 27 NSHSCDTPVDSGYOCFPEISHLMGTSPFSLADESAISPDVPGKRTFVVOVLSRHGARY 86
Db 1 NSHSCDTPVDSGYOCFPEISHLMGTSPFSLADESAISPDVPGKRTFVVOVLSRHGARY 86
QY 87 PTSSASKAYSALEIOLKNTAFKGYAFLKTYNYTLGADDLTPFGEQOQVNSGIRKRY 146
Db 87 PTSSASKAYSALEIOLKNTAFKGYAFLKTYNYTLGADDLTPFGEQOQVNSGIRKRY 146
QY 147 YKALAKIYPPIRASGSDRYIASSEKIEBQSAKLADPAGANPHQASPVIVITPEAGY 206
Db 147 YKALAKIYPPIRASGSDRYIASSEKIEBQSAKLADPAGANPHQASPVIVITPEAGY 206
QY 207 NNTLDHGLCTAFEESELDGDDVEANFTAVFAPPIRARTLHSPVODHTSTNHTLDSNPATFPLNATLYADFS 266
Db 207 NNTLDHGLCTAFEESELDGDDVEANFTAVFAPPIRARTLHSPVODHTSTNHTLDSNPATFPLNATLYADFS 266
QY 267 DTVAARTSDATQLSFCDLFTHDEWIQYDIQSLGKYYGYGAGNPLGPAQGVGFVVELLART 326
Db 267 DTVAARTSDATQLSFCDLFTHDEWIQYDIQSLGKYYGYGAGNPLGPAQGVGFVVELLART 326
QY 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHNTMTWSIFPALGLYNGKPLSTTSV 386
Db 327 LTHSPVODHTSTNHTLDSNPATFPLNATLYADFSHNTMTWSIFPALGLYNGKPLSTTSV 386
QY 387 ESIEETDGYASWTVFAARAYVEMMOCEA-----EKEPLVAVLNDRVVPLHGGVD 439
Db 387 ESIEETDGYASWTVFAARAYVEMMOCEA-----EKEPLVAVLNDRVVPLHGGVD 439
QY 440 KLGRCRDDFVHGLSFARSGGWMECEFA 467
Db 440 KLGRCRDDFVHGLSFARSGGWMECEFA 467

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Search completed: March 20, 2003, 08:24:16
Job time : 1 secs